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Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: markspencer
Timestamp: [year=2009; month=7; day=2; hr=8; min=17; sec=5; ms=90;]
=====

Reviewer Comments:

- 1.
- E249 Order Sequence Error <211> -> <213>; Expected Mandatory
Tag: <212> in SEQID (9)
- E249 Order Sequence Error <211> -> <213>; Expected Mandatory
Tag: <212> in SEQID (10)
- E249 Order Sequence Error <211> -> <213>; Expected Mandatory
Tag: <212> in SEQID (11)
- E249 Order Sequence Error <211> -> <213>; Expected Mandatory
Tag: <212> in SEQID (12)
- E249 Order Sequence Error <211> -> <213>; Expected Mandatory
Tag: <212> in SEQID (13)
- E249 Order Sequence Error <211> -> <213>; Expected Mandatory
Tag: <212> in SEQID (14)
- E249 Order Sequence Error <211> -> <213>; Expected Mandatory
Tag: <212> in SEQID (15)
- E250 Structural Validation Error; Sequence listing may not be
indexable

<210> 9
<211> 527
<213> unknown
<220>
<223> protein p12 of T2 phage
* * * * *

For SEQ ID # 9 through 15, numeric identifier "<212> Type" is mandatory.
Please insert numeric identifier <212>, with the appropriate response,
between numeric identifiers <211> and <213> for each SEQ ID # 9 through

15.

2.

W213	Artificial or Unknown found in <213> in SEQ ID (1)
W213	Artificial or Unknown found in <213> in SEQ ID (2)
W213	Artificial or Unknown found in <213> in SEQ ID (3)
W213	Artificial or Unknown found in <213> in SEQ ID (4)
W213	Artificial or Unknown found in <213> in SEQ ID (5)
W213	Artificial or Unknown found in <213> in SEQ ID (6)
W213	Artificial or Unknown found in <213> in SEQ ID (7)
W213	Artificial or Unknown found in <213> in SEQ ID (8)
W213	Artificial or Unknown found in <213> in SEQ ID (9)
W213	Artificial or Unknown found in <213> in SEQ ID (10)
W213	Artificial or Unknown found in <213> in SEQ ID (11)
W213	Artificial or Unknown found in <213> in SEQ ID (12)
W213	Artificial or Unknown found in <213> in SEQ ID (13)
W213	Artificial or Unknown found in <213> in SEQ ID (14)
W213	Artificial or Unknown found in <213> in SEQ ID (15)

The warnings shown above are ok and require no response.

Application No: 10583415 Version No: 2.0

Input Set:**Output Set:**

Started: 2009-06-24 14:16:41.386
Finished: 2009-06-24 14:16:43.604
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 218 ms
Total Warnings: 15
Total Errors: 8
No. of SeqIDs Defined: 15
Actual SeqID Count: 15

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID (13)

Input Set:

Output Set:

Started: 2009-06-24 14:16:41.386
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Total Warnings: 15
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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
E 249	Order Sequence Error <211> -> <213>; Expected Mandatory Tag: <212> in SEQID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
E 250	Structural Validation Error; Sequence listing may not be indexable

SEQUENCE LISTING

<110> MEYER, ROMAN
 SCHUTZ, MICHAEL
 GRALLERT, HOLGER
 GRASSL, RENATE
 MILLER, STEFAN

<120> ENDOTOXIN DETECTION METHOD

<130> DEBE:067US

<140> 10/583,415

<141> 2006-06-15

<150> PCT/DE2004/002778

<151> 2004-12-20

<150> DE 103 60 844.3

<151> 2003-12-20

<160> 15

<170> PatentIn version 3.3

<210> 1

<211> 78

<212> DNA

<213> artificial sequence

<220>

<223> Synthetic primer

<400> 1

gaaggaacta gtcatatggc tagctggagc caccgcagc tcgaaaaagg cgccagtaat 60

aatacatatc aacacggtt 78

<210> 2

<211> 54

<212> DNA

<213> artificial sequence

<220>

<223> Synthetic primer

<400> 2

acgcgcaaag cttgtcgacg gatcctatca ttcttttacc ttaattatgt agtt 54

<210> 3

<211> 78

<212> DNA

<213> artificial sequence

<220>

<223> Synthetic primer

<400> 3

gaaggaacta gtcatatggc ttgttggagc caccgcagc tcgaaaaagg cgccagtaat 60

aatacatatc aacacgtt 78

<210> 4

<211> 78

<212> DNA

<213> artificial sequence

<220>

<223> Synthetic primer

<400> 4

gaaggaacta gtcatatggc tagctggagc caccgcagc tcgaaaaagg cgccagtaat 60

aatacatatc aacacgtt 78

<210> 5

<211> 19

<212> PRT

<213> artificial sequence

<220>

<223> strep tag

<400> 5

Met Ala Ser Trp Ser His Pro Gln Phe Glu Lys Gly Ala Ser Asn Asn
1 5 10 15

Thr Tyr Gln

<210> 6

<211> 19

<212> PRT

<213> artificial sequence

<220>

<223> strep tag

<400> 6

Met Ala Cys Trp Ser His Pro Gln Phe Glu Lys Gly Ala Ser Asn Asn
1 5 10 15

Thr Tyr Gln

<210> 7
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> strep tag

<400> 7

Met Ala Ser Trp Ser His Pro Gln Phe Glu Lys Gly Ala Cys Asn Asn
1 5 10 15

Thr Tyr Gln

<210> 8
<211> 539
<212> PRT
<213> artificial sequence

<220>
<223> T4p12 with strep tag

<400> 8

Met Ala Ser Trp Ser His Pro Gln Phe Glu Lys Gly Ala Ser Asn Asn
1 5 10 15

Thr Tyr Gln His Val Ser Asn Glu Ser Arg Tyr Val Lys Phe Asp Pro
20 25 30

Thr Asp Thr Asn Phe Pro Pro Glu Ile Thr Asp Val Gln Ala Ala Ile
35 40 45

Ala Ala Ile Ser Pro Ala Gly Val Asn Gly Val Pro Asp Ala Ser Ser
50 55 60

Thr Thr Lys Gly Ile Leu Phe Leu Ala Thr Glu Gln Glu Val Ile Asp
65 70 75 80

Gly Thr Asn Asn Thr Lys Ala Val Thr Pro Ala Thr Leu Ala Thr Arg
85 90 95

Leu Ser Tyr Pro Asn Ala Thr Glu Ala Val Tyr Gly Leu Thr Arg Tyr
100 105 110

<213> artificial sequence

Ser Thr Asp Asp Glu Ala Ile Ala Gly Val Asn Asn Glu Ser Ser Ile
115 120 125

Thr Pro Ala Lys Phe Thr Val Ala Leu Asn Asn Val Phe Glu Thr Arg
130 135 140

Val Ser Thr Glu Ser Ser Asn Gly Val Ile Lys Ile Ser Ser Leu Pro
145 150 155 160

Gln Ala Leu Ala Gly Ala Asp Asp Thr Thr Ala Met Thr Pro Leu Lys
165 170 175

Thr Gln Gln Leu Ala Val Lys Leu Ile Ala Gln Ile Ala Pro Ser Lys
180 185 190

Asn Ala Ala Thr Glu Ser Glu Gln Gly Val Ile Gln Leu Ala Thr Val
195 200 205

Ala Gln Ala Arg Gln Gly Thr Leu Arg Glu Gly Tyr Ala Ile Ser Pro
210 215 220

Tyr Thr Phe Met Asn Ser Thr Ala Thr Glu Glu Tyr Lys Gly Val Ile
225 230 235 240

Lys Leu Gly Thr Gln Ser Glu Val Asn Ser Asn Asn Ala Ser Val Ala
245 250 255

Val Thr Gly Ala Thr Leu Asn Gly Arg Gly Ser Thr Thr Ser Met Arg
260 265 270

Gly Val Val Lys Leu Thr Thr Thr Ala Gly Ser Gln Ser Gly Gly Asp
275 280 285

Ala Ser Ser Ala Leu Ala Trp Asn Ala Asp Val Ile His Gln Arg Gly
290 295 300

Gly Gln Thr Ile Asn Gly Thr Leu Arg Ile Asn Asn Thr Leu Thr Ile
305 310 315 320

Ala Ser Gly Gly Ala Asn Ile Thr Gly Thr Val Asn Met Thr Gly Gly
325 330 335

Tyr Ile Gln Gly Lys Arg Val Val Thr Gln Asn Glu Ile Asp Arg Thr

340	345	350
Ile Pro Val Gly Ala Ile Met Met Trp Ala Ala Asp Ser Leu Pro Ser		
355	360	365
Asp Ala Trp Arg Phe Cys His Gly Gly Thr Val Ser Ala Ser Asp Cys		
370	375	380
Pro Leu Tyr Ala Ser Arg Ile Gly Thr Arg Tyr Gly Gly Ser Ser Ser		
385	390	395 400
Asn Pro Gly Leu Pro Asp Met Arg Gly Leu Phe Val Arg Gly Ser Gly		
405	410	415
Arg Gly Ser His Leu Thr Asn Pro Asn Val Asn Gly Asn Asp Gln Phe		
420	425	430
Gly Lys Pro Arg Leu Gly Val Gly Cys Thr Gly Gly Tyr Val Gly Glu		
435	440	445
Val Gln Lys Gln Gln Met Ser Tyr His Lys His Ala Gly Gly Phe Gly		
450	455	460
Glu Tyr Asp Asp Ser Gly Ala Phe Gly Asn Thr Arg Arg Ser Asn Phe		
465	470	475 480
Val Gly Thr Arg Lys Gly Leu Asp Trp Asp Asn Arg Ser Tyr Phe Thr		
485	490	495
Asn Asp Gly Tyr Glu Ile Asp Pro Ala Ser Gln Arg Asn Ser Arg Tyr		
500	505	510
Thr Leu Asn Arg Pro Glu Leu Ile Gly Asn Glu Thr Arg Pro Trp Asn		
515	520	525
Ile Ser Leu Asn Tyr Ile Ile Lys Val Lys Glu		
530	535	

<210> 9
 <211> 527
 <213> unknown

<220>
 <223> protein p12 of T2 phage

<400> 9

Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Arg Tyr Val
1 5 10 15

Lys Phe Asp Pro Thr Asp Thr Asn Phe Pro Pro Glu Ile Thr Asp Val
20 25 30

Gln Ala Ala Ile Ala Ala Ile Ser Pro Ala Gly Val Asn Gly Val Pro
35 40 45

Asp Ala Ser Ser Thr Thr Lys Gly Ile Leu Phe Leu Ala Thr Glu Gln
50 55 60

Glu Val Ile Asp Gly Thr Asn Asn Thr Lys Ala Val Thr Pro Ala Thr
65 70 75 80

Leu Ala Thr Arg Leu Ser Tyr Pro Asn Ala Thr Glu Ala Val Tyr Gly
85 90 95

Leu Thr Arg Tyr Ser Thr Asp Asp Glu Ala Ile Ala Gly Val Asn Asn
100 105 110

Glu Ser Ser Ile Thr Pro Ala Lys Phe Thr Val Ala Leu Asn Asn Val
115 120 125

Phe Glu Thr Arg Val Ser Thr Glu Ser Ser Asn Gly Val Ile Lys Ile
130 135 140

Ser Ser Leu Pro Gln Ala Leu Ala Gly Ala Asp Asp Thr Thr Ala Met
145 150 155 160

Thr Pro Leu Lys Thr Gln Gln Leu Ala Val Lys Leu Ile Ala Gln Ile
165 170 175

Ala Pro Ser Lys Asn Ala Ala Thr Glu Ser Glu Gln Gly Val Ile Gln
180 185 190

Leu Ala Thr Val Ala Gln Ala Arg Gln Gly Thr Leu Arg Glu Gly Tyr
195 200 205

Ala Ile Ser Pro Tyr Thr Phe Met Asn Ser Thr Ala Thr Glu Glu Tyr
210 215 220

Lys Gly Val Ile Lys Leu Gly Thr Gln Ser Glu Val Asn Ser Asn Asn
225 230 235 240

Ala Ser Val Ala Val Thr Gly Ala Thr Leu Asn Gly Arg Gly Ser Thr
245 250 255

Thr Ser Met Arg Gly Val Val Lys Leu Thr Thr Thr Ala Gly Ser Gln
260 265 270

Ser Gly Gly Asp Ala Ser Ser Ala Leu Ala Trp Asn Ala Asp Val Ile
275 280 285

His Gln Arg Gly Gly Gln Thr Ile Asn Gly Thr Leu Arg Ile Asn Asn
290 295 300

Thr Leu Thr Ile Ala Ser Gly Gly Ala Asn Ile Thr Gly Thr Val Asn
305 310 315 320

Met Thr Gly Gly Tyr Ile Gln Gly Lys Arg Val Val Thr Gln Asn Glu
325 330 335

Ile Asp Arg Thr Ile Pro Val Gly Ala Ile Met Met Trp Ala Ala Asp
340 345 350

Ser Leu Pro Ser Asp Ala Trp Arg Phe Cys His Gly Gly Thr Val Ser
355 360 365

Ala Ser Asp Cys Pro Leu Tyr Ala Ser Arg Ile Gly Thr Arg Tyr Gly
370 375 380

Gly Thr Ser Ser Asn Pro Gly Leu Pro Asp Met Arg Gly Leu Phe Val
385 390 395 400

Arg Gly Ser Gly Arg Gly Ser His Leu Thr Asn Pro Asn Val Asn Gly
405 410 415

Asn Asp Gln Phe Gly Lys Pro Arg Leu Gly Val Gly Cys Thr Gly Gly
420 425 430

Tyr Val Gly Glu Val Gln Lys Gln Gln Met Ser Tyr His Lys His Ala
435 440 445

Gly Gly Phe Gly Glu Tyr Asp Asp Ser Gly Ala Phe Gly Asn Thr Arg
450 455 460

Arg Ser Asn Phe Val Gly Thr Arg Lys Gly Leu Asp Trp Asp Asn Arg
465 470 475 480

Ser Tyr Phe Thr Asn Asp Gly Tyr Glu Ile Asp Pro Ala Ser Gln Arg
485 490 495

Asn Ser Arg Tyr Thr Leu Asn Arg Pro Glu Leu Ile Gly Asn Glu Thr
500 505 510

Arg Pro Trp Asn Ile Ser Leu Asn Tyr Ile Ile Lys Val Lys Glu
515 520 525

<210> 10
<211> 527
<213> unknown

<220>
<223> protein p12 of T4 phage

<400> 10

Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Arg Tyr Val
1 5 10 15

Lys Phe Asp Pro Thr Asp Thr Asn Phe Pro Pro Glu Ile Thr Asp Val
20 25 30

His Ala Ala Ile Ala Ala Ile Ser Pro Ala Gly Val Asn Gly Val Pro
35 40 45

Asp Ala Ser Ser Thr Thr Lys Gly Ile Leu Phe Ile Pro Thr Glu Gln
50 55 60

Glu Val Ile Asp Gly Thr Asn Asn Thr Lys Ala Val Thr Pro Ala Thr
65 70 75 80

Leu Ala Thr Arg Leu Ser Tyr Pro Asn Ala Thr Glu Thr Val Tyr Gly
85 90 95

Leu Thr Arg Tyr Ser Thr Asn Asp Glu Ala Ile Ala Gly Val Asn Asn
100 105 110

Glu	Ser	Ser	Ile	Thr	Pro	Ala	Lys	Phe	Thr	Val	Ala	Leu	Asn	Asn	Ala	
		115					120					125				
Phe	Glu	Thr	Arg	Val	Ser	Thr	Glu	Ser	Ser	Asn	Gly	Val	Ile	Lys	Ile	
	130					135					140					
Ser	Ser	Leu	Pro	Gln	Ala	Leu	Ala	Gly	Ala	Asp	Asp	Thr	Thr	Ala	Met	
145					150					155					160	
Thr	Pro	Leu	Lys	Thr	Gln	Gln	Leu	Ala	Ile	Lys	Leu	Ile	Ala	Gln	Ile	
				165					170					175		
Ala	Pro	Ser	Glu	Thr	Thr	Ala	Thr	Glu	Ser	Asp	Gln	Gly	Val	Val	Gln	
			180					185					190			
Leu	Ala	Thr	Val	Ala	Gln	Val	Arg	Gln	Gly	Thr	Leu	Arg	Glu	Gly	Tyr	
		195					200					205				
Ala	Ile	Ser	Pro	Tyr	Thr	Phe	Met	Asn	Ser	Ser	Ser	Thr	Glu	Glu	Tyr	
	210					215					220					
Lys	Gly	Val	Ile	Lys	Leu	Gly	Thr	Gln	Ser	Glu	Val	Asn	Ser	Asn	Asn	
225					230					235					240	
Ala	Ser	Val	Ala	Val	Thr	Gly	Ala	Thr	Leu	Asn	Gly	Arg	Gly	Ser	Thr	
				245					250					255		
Thr	Ser	Met	Arg	Gly	Val	Val	Lys	Leu	Thr	Thr	Thr	Ala	Gly	Ser	Gln	
			260					265					270			
Ser	Gly	Gly	Asp	Ala	Ser	Ser	Ala	Leu	Ala	Trp	Asn	Ala	Asp	Val	Ile	
		275					280					285				
Gln	Gln	Arg	Gly	Gly	Gln	Ile	Ile	Tyr	Gly	Thr	Leu	Arg	Ile	Glu	Asp	
		290				295					300					
Thr	Phe	Thr	Ile	Ala	Asn	Gly	Gly	Ala	Asn	Ile	Thr	Gly	Thr	Val	Arg	
305					310					315					320	
Met	Thr	Gly	Gly	Tyr	Ile	Gln	Gly	Asn	Arg	Ile	Val	Thr	Gln	Asn	Glu	
				325					330					335		

Ile Asp Arg Thr Ile Pro Val Gly Ala Ile Met Met Trp Ala Ala Asp
340 345 350

Ser Leu Pro Ser Asp Ala Trp Arg Phe Cys His Gly Gly Thr Val Ser
355 360 365

Ala Ser Asp Cys Pro Leu Tyr Ala Ser Arg Ile Gly Thr Arg Tyr Gly
370 375 380

Gly Asn Pro Ser Asn Pro Gly Leu Pro Asp Met Arg Gly Leu Phe Val
385 390 395 400

Arg Gly Ser Gly Arg Gly Ser His Leu Thr Asn Pro Asn Val Asn Gly
405 410 415

Asn Asp Gln Phe Gly Lys Pro Arg Leu Gly Val Gly Cys Thr Gly Gly
420 425 430

Tyr Val Gly Glu Val Gln Ile Gln Gln Met Ser Tyr His Lys His Ala
435 440 445

Gly Gly Phe Gly Glu His Asp Asp Leu Gly Ala Phe Gly Asn Thr Arg
450 455 460

Arg Ser Asn Phe Val Gly Thr Arg Lys Gly Leu Asp Trp Asp Asn Arg
465 470 475 480

Ser Tyr Phe Thr Asn Asp Gly Tyr Glu Ile Asp Pro Glu Ser Gln Arg
485 490 495

Asn Ser Lys Tyr Thr Leu Asn Arg Pro Glu Leu Ile Gly Asn Glu Thr
500 505 510

Arg Pro Trp Asn Ile Ser Leu Asn Tyr Ile Ile Lys Val Lys Glu
515 520 525

<210> 11

<211> 518

<213> unknown

<220>

<223> protein p12 of PP01 phage

<400> 11

Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Lys Tyr Val
1 5 10 15

Lys Phe Asp Pro Val Gly Ser Asn Phe Pro Asp Thr Val Thr Thr Val
20 25 30

Gln Ser Ala Leu Ser Lys Ile Ser Asn Ile Gly Val Asn Gly Ile Pro
35 40 45

Asp Ala Ser Met Glu Val Lys Gly Ile Ala Met Ile Ala Ser Glu Gln
50 55 60

Glu Val Leu Asp Gly Thr Asn Asn Ser Lys Ile Val Thr Pro Ala Thr
65 70 75 80

Leu Ala Thr Arg Leu Leu Tyr Pro Asn Ala Thr Glu Thr Lys Tyr Gly
85 90 95

Leu Thr Arg Tyr Ser Thr Asn Glu Glu Thr Leu Glu Gly Ser Asp Asn
100 105 110

Asn Ser Ser Ile Thr Pro Gln Lys Leu Lys Tyr His Thr Asp Asp Val
115 120 125

Phe Gln Asn Arg Tyr Ser Ser Glu Ser Ser Asn Gly Val Ile Lys Ile
130 135 140

Ser Ser Thr Pro Ala Ala Leu Ala Gly Val Asp Asp Thr Thr Ala Met
145 150 155 160

Thr Pro Leu Lys Thr Gln Lys Leu Ala Ile Lys Leu Ile Ser Gln Ile
165 170 175

Ala Pro Ser Glu Asp Thr Ala Ser Glu Ser Val Arg Gly Val Val Gln
180 185 190

Leu Ser Thr Val Ala Gln Thr Arg Gln Gly Thr Leu Arg Glu Gly Tyr
195 200 205

Ala Ile Ser Pro Tyr Thr Phe Met Asn Ser Val Ala Thr Gln Glu Tyr
210 215 220

Lys Gly Val Ile Arg Leu Gly Thr Gln Ser Glu Ile Asn Ser Asn Leu

225

230

235

240

Gly Asp Val Ala Val Thr Gly Glu Thr Leu Asn Gly Arg Gly Ala Thr
245 250 255

Gly Ser Met Arg Gly Val Val Lys Leu Thr Thr Gln Ala Gly Ile Ala
260 265 270